

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical
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Application Serial Number: 10/809,144
Source: IFWD
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IFWO

RAW SEQUENCE LISTING

DATE: 10/18/2004

PATENT APPLICATION: US/10/809,144

TIME: 13:56:18

Input Set : A:\03-284-E.ST25.txt

Output Set: N:\CRF4\10182004\J809144.raw

```

3 <110> APPLICANT: The Board of Trustees of the University of Illinois
4      Costa, Robert
5      Raychaudhuri, Pradip
6      Wang, Xinhe
7      Kalinichenko, Vladimir
8      Major, Michael
9      Wang, I-Ching
11 <120> TITLE OF INVENTION: METHODS OF INHIBITING TUMOR CELL PROLIFERATION
13 <130> FILE REFERENCE: 03-284-E
15 <140> CURRENT APPLICATION NUMBER: US 10/809,144
16 <141> CURRENT FILING DATE: 2004-03-25
18 <150> PRIOR APPLICATION NUMBER: US 60/457,257
19 <151> PRIOR FILING DATE: 2003-03-25
21 <150> PRIOR APPLICATION NUMBER: US 60/474,075
22 <151> PRIOR FILING DATE: 2003-10-23
24 <150> PRIOR APPLICATION NUMBER: US 60/540,691
25 <151> PRIOR FILING DATE: 2004-01-30
27 <150> PRIOR APPLICATION NUMBER: US 60/549,691
28 <151> PRIOR FILING DATE: 2004-03-02
30 <160> NUMBER OF SEQ ID NOS: 13
32 <170> SOFTWARE: PatentIn version 3.0
34 <210> SEQ ID NO: 1
35 <211> LENGTH: 2737
36 <212> TYPE: DNA
37 <213> ORGANISM: Homo Sapiens
39 <400> SEQUENCE: 1
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42 ggtccacact tgtgattctc aatggagagt gaaaacgcag attcataatg aaaactagcc      120
44 ccgctcggcc actgattctc aaaagacgga ggctgcccct tcctgttcaa aatgccccaa      180
46 gtgaaacatc agaggaggaa cctaagagat cccctgcccc acaggagtct aatcaagcag      240
48 aggcctccaa ggaagtggca gagtccaact cttgcaagtt tccagctggg atcaagatta      300
50 ttaaccaccc caccatgccc aacacgcaag tagtggccat cccaacaat gctaataatc      360
52 acagcatcat cacagactg actgccaagg gaaaagagag tggcagtagt gggcccaaca      420
54 aattcatcct catcagctgt gggggagccc caactcagcc tccaggactc cggcctcaaa      480
56 cccaaccag ctatgatgcc aaaaggacag aagtgaccct ggagaccttg ggaccaaaac      540
58 ctgcagctag ggatgtgaat ctctctagac cacctggagc cctttgcgag cagaaacggg      600
60 agacctgtgc agatggtagc gcagcaggct gcactatcaa caatagccta tccaacatcc      660
62 agtggcttcg aaagatgagt tctgatggac tgggctcccc cagcatcaag caagagatgg      720
64 aggaaaagga gaattgtcac ctggagcagc gacagggttaa ggttgaggag ccttcgagac      780
66 catcagcgtc ctggcagaac tctgtgtctg agcggccacc ctactcttac atggccatga      840
68 tacaattcgc catcaacagc actgagagga agcgcagtac tttgaaagac atctatacgt      900
70 ggattgagga ccactttccc tactttaagc acattgccaa gccaggctgg aagaactcca      960
72 tccgccacaa cctttccctg caccgacatgt ttgtccggga gacgtctgcc aatggcaagg      1020

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74 tctccttctg gaccattcac cccagtgcc accgctactt gacattggac caggtgttta 1080
76 agcagcagaa acgaccgaat ccagagctcc gccggaacat gaccatcaaa accgaactcc 1140
78 ccctgggccc acggcggaag atgaagccac tgctaccacg ggtcagctca tacctggtag 1200
80 ctatccagtt cccggtgaac cagtcactgg tgttcagacc ctccggtgaag gtgccattgc 1260
82 ccctggcggc ttccctcatg agctcagagc ttgcccgcca tagcaagcga gtccgcattg 1320
84 cccccaaggt gctgctagct gaggagggga tagctcctct ttcttctgca ggaccaggga 1380
86 aagaggagaa actcctgttt ggagaagggt tttctccttt gcttccagtt cagactatca 1440
88 aggaggaaga aatccagcct ggggaggaaa tgccacactt agcgagaccc atcaaagtgg 1500
90 agagccctcc cttggaagag tggccctccc cggcccccac tttcaaagag gaatcatctc 1560
92 actcctggga ggattcgtcc caatctccca cccaagacc caagaagtcc tacagtgggc 1620
94 ttaggtcccc aaccgggtgt gtctcgaaa tgcttgtgat tcaacacagg gagaggaggg 1680
96 agaggagccg gtctcggagg aaacagcatc tactgcctcc ctgtgtggat gagccggagc 1740
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100 actcctctga cctgcctccc cagctcagct actcccagga agtgggagga ccttttaaga 1860
102 caccatttaa ggaaacgtg cccatctcct ccaccccgag caaatctgtc ctcccagaa 1920
104 cccctgaatc ctggaggctc acgccccag ccaaagtagg gggactggat ttcagcccag 1980
106 taaaaacctc ccagggtgcc tctgacctct tgcccgacc cctggggctg atggatctca 2040
108 gcaccactcc cttgcaaagt gtcctccccc ttgaatcacc gcaaaggctc ctcaattcag 2100
110 aacccttaga cctcatctcc gtcccttttg gcaactcttc tccctcagat atagacgtcc 2160
112 ccaagccagg ctccccggag ccacaggttt ctggccttgc agccaatcgt tctctgacag 2220
114 aaggcctggt cctggacaca atgaatgaca gcctcagcaa gatcctgctg gacatcagct 2280
116 ttcttgccct ggacaggac ccactgggcc ctgacaacat caactggctc cagtttattc 2340
118 ctgagctaca gtagagccct gcccttgccc ctgtgctcaa gctgtccacc atcccgggca 2400
120 ctccaaggct cagtgcaccc caagcctctg agtgaggaca gcaggcaggg actgttctgc 2460
122 tcctcatagc tccctgctgc ctgattatgc aaaagtagca gtcacaccct agccactgct 2520
124 gggaccttgt gttccccaag agtatctgat tcctctgctg tccctgccag gagctgaagg 2580
126 gtgggaacaa caaaggcaat ggtgaaaaga gattaggaac cccccagcct gtttccattc 2640
128 tctgcccagc agtctcttac ctccctgat ctttgcaggg tggctcctgt aaatagtata 2700
130 aattctccaa attatcctct aattataaat gtaagct 2737

```

133 <210> SEQ ID NO: 2

134 <211> LENGTH: 748

135 <212> TYPE: PRT

136 <213> ORGANISM: Homo sapiens

138 <400> SEQUENCE: 2

```

140 Met Lys Thr Ser Pro Arg Arg Pro Leu Ile Leu Lys Arg Arg Arg Leu
141 1 5 10 15
143 Pro Leu Pro Val Gln Asn Ala Pro Ser Glu Thr Ser Glu Glu Glu Pro
144 20 25 30
146 Lys Arg Ser Pro Ala Gln Gln Glu Ser Asn Gln Ala Glu Ala Ser Lys
147 35 40 45
149 Glu Val Ala Glu Ser Asn Ser Cys Lys Phe Pro Ala Gly Ile Lys Ile
150 50 55 60
152 Ile Asn His Pro Thr Met Pro Asn Thr Gln Val Val Ala Ile Pro Asn
153 65 70 75 80
155 Asn Ala Asn Ile His Ser Ile Ile Thr Ala Leu Thr Ala Lys Gly Lys
156 85 90 95
158 Glu Ser Gly Ser Ser Gly Pro Asn Lys Phe Ile Leu Ile Ser Cys Gly
159 100 105 110
161 Gly Ala Pro Thr Gln Pro Pro Gly Leu Arg Pro Gln Thr Gln Thr Ser

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162          115          120          125
164 Tyr Asp Ala Lys Arg Thr Glu Val Thr Leu Glu Thr Leu Gly Pro Lys
165          130          135          140
167 Pro Ala Ala Arg Asp Val Asn Leu Pro Arg Pro Pro Gly Ala Leu Cys
168 145          150          155          160
170 Glu Gln Lys Arg Glu Thr Cys Ala Asp Gly Glu Ala Ala Gly Cys Thr
171          165          170          175
173 Ile Asn Asn Ser Leu Ser Asn Ile Gln Trp Leu Arg Lys Met Ser Ser
174          180          185          190
176 Asp Gly Leu Gly Ser Arg Ser Ile Lys Gln Glu Met Glu Glu Lys Glu
177          195          200          205
179 Asn Cys His Leu Glu Gln Arg Gln Val Lys Val Glu Glu Pro Ser Arg
180          210          215          220
182 Pro Ser Ala Ser Trp Gln Asn Ser Val Ser Glu Arg Pro Pro Tyr Ser
183 225          230          235          240
185 Tyr Met Ala Met Ile Gln Phe Ala Ile Asn Ser Thr Glu Arg Lys Arg
186          245          250          255
188 Met Thr Leu Lys Asp Ile Tyr Thr Trp Ile Glu Asp His Phe Pro Tyr
189          260          265          270
191 Phe Lys His Ile Ala Lys Pro Gly Trp Lys Asn Ser Ile Arg His Asn
192          275          280          285
194 Leu Ser Leu His Asp Met Phe Val Arg Glu Thr Ser Ala Asn Gly Lys
195          290          295          300
197 Val Ser Phe Trp Thr Ile His Pro Ser Ala Asn Arg Tyr Leu Thr Leu
198 305          310          315          320
200 Asp Gln Val Phe Lys Gln Gln Lys Arg Pro Asn Pro Glu Leu Arg Arg
201          325          330          335
203 Asn Met Thr Ile Lys Thr Glu Leu Pro Leu Gly Ala Arg Arg Lys Met
204          340          345          350
206 Lys Pro Leu Leu Pro Arg Val Ser Ser Tyr Leu Val Pro Ile Gln Phe
207          355          360          365
209 Pro Val Asn Gln Ser Leu Val Leu Gln Pro Ser Val Lys Val Pro Leu
210          370          375          380
212 Pro Leu Ala Ala Ser Leu Met Ser Ser Glu Leu Ala Arg His Ser Lys
213 385          390          395          400
215 Arg Val Arg Ile Ala Pro Lys Val Leu Leu Ala Glu Glu Gly Ile Ala
216          405          410          415
218 Pro Leu Ser Ser Ala Gly Pro Gly Lys Glu Glu Lys Leu Leu Phe Gly
219          420          425          430
221 Glu Gly Phe Ser Pro Leu Leu Pro Val Gln Thr Ile Lys Glu Glu Glu
222          435          440          445
224 Ile Gln Pro Gly Glu Glu Met Pro His Leu Ala Arg Pro Ile Lys Val
225          450          455          460
227 Glu Ser Pro Pro Leu Glu Glu Trp Pro Ser Pro Ala Pro Ser Phe Lys
228 465          470          475          480
230 Glu Glu Ser Ser His Ser Trp Glu Asp Ser Ser Gln Ser Pro Thr Pro
231          485          490          495
233 Arg Pro Lys Lys Ser Tyr Ser Gly Leu Arg Ser Pro Thr Arg Cys Val
234          500          505          510

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236 Ser Glu Met Leu Val Ile Gln His Arg Glu Arg Arg Glu Arg Ser Arg
237          515          520          525
239 Ser Arg Arg Lys Gln His Leu Leu Pro Pro Cys Val Asp Glu Pro Glu
240          530          535          540
242 Leu Leu Phe Ser Glu Gly Pro Ser Thr Ser Arg Trp Ala Ala Glu Leu
243 545          550          555          560
245 Pro Phe Pro Ala Asp Ser Ser Asp Pro Ala Ser Gln Leu Ser Tyr Ser
246          565          570          575
248 Gln Glu Val Gly Gly Pro Phe Lys Thr Pro Ile Lys Glu Thr Leu Pro
249          580          585          590
251 Ile Ser Ser Thr Pro Ser Lys Ser Val Leu Pro Arg Thr Pro Glu Ser
252          595          600          605
254 Trp Arg Leu Thr Pro Pro Ala Lys Val Gly Gly Leu Asp Phe Ser Pro
255          610          615          620
257 Val Gln Thr Ser Gln Gly Ala Ser Asp Pro Leu Pro Asp Pro Leu Gly
258 625          630          635          640
260 Leu Met Asp Leu Ser Thr Thr Pro Leu Gln Ser Ala Pro Pro Leu Glu
261          645          650          655
263 Ser Pro Gln Arg Leu Leu Ser Ser Glu Pro Leu Asp Leu Ile Ser Val
264          660          665          670
266 Pro Phe Gly Asn Ser Ser Pro Ser Asp Ile Asp Val Pro Lys Pro Gly
267          675          680          685
269 Ser Pro Glu Pro Gln Val Ser Gly Leu Ala Ala Asn Arg Ser Leu Thr
270          690          695          700
272 Glu Gly Leu Val Leu Asp Thr Met Asn Asp Ser Leu Ser Lys Ile Leu
273 705          710          715          720
275 Leu Asp Ile Ser Phe Pro Gly Leu Asp Glu Asp Pro Leu Gly Pro Asp
276          725          730          735
278 Asn Ile Asn Trp Ser Gln Phe Ile Pro Glu Leu Gln
279          740          745

```

281 <210> SEQ ID NO: 3

282 <211> LENGTH: 6

283 <212> TYPE: PRT

284 <213> ORGANISM: Artificial

286 <220> FEATURE:

287 <223> OTHER INFORMATION: FoxM1B LXLXXL motif

289 <220> FEATURE:

290 <221> NAME/KEY: UNSURE

291 <222> LOCATION: (2)..(2)

292 <223> OTHER INFORMATION: X is any amino acid

295 <220> FEATURE:

296 <221> NAME/KEY: UNSURE

297 <222> LOCATION: (4)..(5)

298 <223> OTHER INFORMATION: X is any amino acid

301 <400> SEQUENCE: 3

W--> 303 Leu Xaa Leu Xaa Xaa Leu

304 1 5

306 <210> SEQ ID NO: 4

307 <211> LENGTH: 66

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Input Set : A:\03-284-E.ST25.txt

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308 <212> TYPE: DNA
309 <213> ORGANISM: Artificial
311 <220> FEATURE:
312 <223> OTHER INFORMATION: EcoR1 T-epitope tagged FoxM1B primer
314 <400> SEQUENCE: 4
315 gcggaattca ccatggctag catgactggg ggacagcaaa tggggtggca gaactctgtg      60
317 tctgag                                                                66
320 <210> SEQ ID NO: 5
321 <211> LENGTH: 18
322 <212> TYPE: DNA
323 <213> ORGANISM: Artificial
325 <220> FEATURE:
326 <223> OTHER INFORMATION: antisense primer for CMV expression vector SV-40 poly A
region
328 <400> SEQUENCE: 5
329 gtttgtccaa ttatgtca                                                    18
332 <210> SEQ ID NO: 6
333 <211> LENGTH: 12
334 <212> TYPE: DNA
335 <213> ORGANISM: Artificial
337 <220> FEATURE:
338 <223> OTHER INFORMATION: FoxM1B/FoxA binding site
340 <400> SEQUENCE: 6
341 tttgtttggt tg                                                        12
344 <210> SEQ ID NO: 7
345 <211> LENGTH: 6
346 <212> TYPE: RNA
347 <213> ORGANISM: Artificial
349 <220> FEATURE:
350 <223> OTHER INFORMATION: transcription termination signal
352 <400> SEQUENCE: 7
353 aauaaa                                                                6
356 <210> SEQ ID NO: 8
357 <211> LENGTH: 81
358 <212> TYPE: PRT
359 <213> ORGANISM: Homo sapiens
361 <400> SEQUENCE: 8
363 Pro Phe Lys Thr Pro Ile Lys Glu Thr Leu Pro Ile Ser Ser Thr Pro
364 1          5          10          15
366 Ser Lys Ser Val Leu Pro Arg Thr Pro Glu Ser Trp Arg Leu Thr Pro
367          20          25          30
369 Pro Ala Lys Val Gly Gly Leu Asp Phe Ser Pro Val Gln Thr Ser Gln
370          35          40          45
372 Gly Ala Ser Asp Pro Leu Pro Asp Pro Leu Gly Leu Met Asp Leu Ser
373          50          55          60
375 Thr Thr Pro Leu Gln Ser Ala Pro Pro Leu Glu Ser Pro Gln Arg Leu
376 65          70          75          80
378 Leu
381 <210> SEQ ID NO: 9
382 <211> LENGTH: 28

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/809,144

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Input Set : A:\03-284-E.ST25.txt
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; Xaa Pos. 2,4,5

Seq#:9; Xaa Pos. 2,3,4,6,8,9,11,12,13,14,16,17,18,19,20,22,23,24,25,26

Seq#:10; Xaa Pos. 1,2,3,4,5,6,7,8,9

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:3,4,5,6,7,9

VERIFICATION SUMMARY

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Input Set : A:\03-284-E.ST25.txt

Output Set: N:\CRF4\10182004\J809144.raw

L:303 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0
L:427 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:0
M:341 Repeated in SeqNo=9
L:446 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:0